

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph starting at page 49 line 4 to read as follows:

Nucleic acid sequences that encode putative  $\Delta 6$ -desaturases were identified through a BLASTX search of the Expressed Sequence Tag ("EST") databases through NCBI using the Ma524 amino acid sequence. Several sequences showed significant homology. In particular, the deduced amino acid sequence of two *Arabidopsis thaliana* sequences, (accession numbers F13728 and T42806) showed homology to two different regions of the deduced amino acid sequence of Ma524. The following PCR primers were designed: ATTS4723-FOR (complementary to F13728) SEQ ID NO:13 5' CUACUACUACUAGGAGTCCTCTACGGTGTTTTG and T42806-REV (complementary to T42806) SEQ ID NO:14 5' CAUCAUCAUATGATGCTCAAGCTGAACTG. Five  $\mu$ g of total RNA isolated from developing siliques of *Arabidopsis thaliana* was reverse transcribed using BRL Superscript RTase and the primer TSyn (5'-CCAAGCTTCTGCAGGAGCTCTTTTTTTTTTTTTTTT-3') and is shown as SEQ ID NO:12. PCR was carried out in a 50  $\mu$ l volume containing: template derived from 25 ng total RNA, 2 pM each primer, 200  $\mu$ M each deoxyribonucleotide triphosphate, 60 mM Tris-HCl, pH 8.5, 15 mM  $(\text{NH}_4)_2\text{SO}_4$ , 2 mM  $\text{MgCl}_2$ , 0.2 U Taq Polymerase. Thermocycler conditions were as follows: 94 degrees for 30 sec., 50 degrees for 30 sec., 72 degrees for 30 sec. PCR was continued for 35 cycles followed by an additional extension at 72 degrees for 7 minutes. PCR resulted in a fragment of approximately ~750 base pairs which was subcloned, named 12-5, and sequenced. Each end of this fragment was formed to correspond to the *Arabidopsis* ESTs from which the PCR primers were designed. The putative amino acid sequence of 12-5 was compared to that of Ma524, and ESTs from human (W28140), mouse (W53753), and *C. elegans* (R05219) (see Figure 4). Homology patterns with the *Mortierella*  $\Delta 6$ -desaturase indicate that these sequences represent putative desaturase polypeptides. Based on this experiment approach, it is likely that the full-length genes can be cloned using probes based on the EST sequences. Following the cloning, the genes can then be placed into expression vectors, expressed in host cells, and their specific  $\Delta 6$ - or other desaturase activity can be determined as described below.